

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099

DATE: 05/19/2000
TIME: 07:33:01

INPUT SET: S35499.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Barry, Gerard F.
Kishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.

(ii) TITLE OF INVENTION: Glyphosate Tolerant
5-Enolpyruvylshikimate-3-Phosphate Synthases

(iii) NUMBER OF SEQUENCES: 69

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
(B) STREET: 700 Chesterfield Village Parkway
(C) CITY: St. Louis
(D) STATE: Missouri
(E) COUNTRY: USA
(F) ZIP: 63198

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/464,099
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/137,440
(B) FILING DATE:

(A) APPLICATION NUMBER: US 08/833,485
(B) FILING DATE: 07-APR-1997

(A) APPLICATION NUMBER: US 08/306,063
(B) FILING DATE: 13-SEP-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/749,611

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TIME: 07:33:02

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47 (B) FILING DATE: 28-AUG-1991
48
49
50 (vii) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: US 07/576,537
52 (B) FILING DATE: 31-AUG-1990
53
54
55 (viii) ATTORNEY/AGENT INFORMATION:
56 (A) NAME: Hoerner Jr., Dennis R.
57 (B) REGISTRATION NUMBER: 30,914
58 (C) REFERENCE/DOCKET NUMBER: 38-21(15117)A
59
60 (ix) TELECOMMUNICATION INFORMATION:
61 (A) TELEPHONE: (314)737-6099
62 (B) TELEFAX: (314)737-6047
63
64
65 (2) INFORMATION FOR SEQ ID NO:1:
66
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 597 base pairs
69 (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: double
71 (D) TOPOLOGY: linear
72
73 (ii) MOLECULE TYPE: DNA (genomic)
74
75
76
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
78
79 TCATCAAAAT ATTTAGCAGC ATTCCAGATT GGGTTCAATC AACAAAGGTAC GAGCCATATC 60
80
81 ACTTTATTCA AATTGGTATC GCCAAAACCA AGAAGGAACT CCCATCCTCA AAGGTTTGTA 120
82
83 AGGAAGAATT CTCAGTCCAA AGCCTCAACA AGGTCAGGGT ACAGAGTCTC CAAACCATTA 180
84
85 GCCAAAAGCT ACAGGAGATC AATGAAGAAT CTTCAATCAA AGTAAACTAC TGTTCCAGCA 240
86
87 CATGCATCAT GGTCAAGTAAG TTTCAGAAAA AGACATCCAC CGAAGACTTA AAGTTAGTGG 300
88
89 GCATCTTTGA AAGTAATCTT GTCAACATCG AGCAGCTGGC TTGTGGGGAC CAGACAAAAA 360
90
91 AGGAATGGTG CAGAATTGTT AGGCGCACCT ACCAAAAGCA TCTTTGCCTT TATTGCAAAG 420
92
93 ATAAAGCAGA TTCCTCTAGT ACAAGTGGGG AACAAAATAA CGTGGAAAAG AGCTGTCCTG 480
94
95 ACAGCCCACT CACTAATGCG TATGACGAAC GCAGTGACGA CCACAAAAGA ATTCCCTCTA 540
96
97 TATAAGAAGG CATTCAATCC CATTTGAAGG ATCATCAGAT ACTAACCAAT ATTTCTC 597
98
99 (2) INFORMATION FOR SEQ ID NO:2:

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100
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 1982 base pairs
103 (B) TYPE: nucleic acid
104 (C) STRANDEDNESS: double
105 (D) TOPOLOGY: linear
106
107 (ii) MOLECULE TYPE: DNA (genomic)
108
109
110 (ix) FEATURE:
111 (A) NAME/KEY: CDS
112 (B) LOCATION: 62..1426
113
114
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
116
117 AAGCCCGCGT TCTCTCCGGC GCTCCGCCCG GAGAGCCGTG GATAGATTAA GGAAGACGCC 60
118
119 C ATG TCG CAC GGT GCA AGC AGC CGG CCC GCA ACC GCC CGC AAA TCC 106
120 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser
121 1 5 10 15
122
123 TCT GGC CTT TCC GGA ACC GTC CGC ATT CCC GGC GAC AAG TCG ATC TCC 154
124 Ser Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser
125 20 25 30
126
127 CAC CGG TCC TTC ATG TTC GGC GGT CTC GCG AGC GGT GAA ACG CGC ATC 202
128 His Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile
129 35 40 45
130
131 ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC AAT ACG GGC AAG GCC ATG 250
132 Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met
133 50 55 60
134
135 CAG GCC ATG GGC GCC AGG ATC CGT AAG GAA GGC GAC ACC TGG ATC ATC 298
136 Gln Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile
137 65 70 75
138
139 GAT GGC GTC GGC AAT GGC GGC CTC CTG GCG CCT GAG GCG CCG CTC GAT 346
140 Asp Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp
141 80 85 90 95
142
143 TTC GGC AAT GCC GCC ACG GGC TGC CGC CTG ACC ATG GGC CTC GTC GGG 394
144 Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly
145 100 105 110
146
147 GTC TAC GAT TTC GAC AGC ACC TTC ATC GGC GAC GCC TCG CTC ACA AAG 442
148 Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys
149 115 120 125
150
151 CGC CCG ATG GGC CGC GTG TTG AAC CCG CTG CGC GAA ATG GGC GTG CAG 490
152 Arg Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln

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153	130	135	140	
154				
155	GTG AAA TCG GAA GAC GGT GAC CGT CTT CCC GTT ACC TTG CGC GGG CCG			538
156	Val Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro			
157	145	150	155	
158				
159	AAG ACG CCG ACG CCG ATC ACC TAC CGC GTG CCG ATG GCC TCC GCA CAG			586
160	Lys Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln			
161	160	165	170	175
162				
163	GTG AAG TCC GCC GTG CTG CTC GCC GGC CTC AAC ACG CCC GGC ATC ACG			634
164	Val Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr			
165	180	185	190	
166				
167	ACG GTC ATC GAG CCG ATC ATG ACG CGC GAT CAT ACG GAA AAG ATG CTG			682
168	Thr Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu			
169	195	200	205	
170				
171	CAG GGC TTT GGC GCC AAC CTT ACC GTC GAG ACG GAT GCG GAC GGC GTG			730
172	Gln Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val			
173	210	215	220	
174				
175	CGC ACC ATC CGC CTG GAA GGC CGC GGC AAG CTC ACC GGC CAA GTC ATC			778
176	Arg Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile			
177	225	230	235	
178				
179	GAC GTG CCG GGC GAC CCG TCC TCG ACG GCC TTC CCG CTG GTT GCG GCC			826
180	Asp Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala			
181	240	245	250	255
182				
183	CTG CTT GTT CCG GGC TCC GAC GTC ACC ATC CTC AAC GTG CTG ATG AAC			874
184	Leu Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn			
185	260	265	270	
186				
187	CCC ACC CGC ACC GGC CTC ATC CTG ACG CTG CAG GAA ATG GGC GCC GAC			922
188	Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp			
189	275	280	285	
190				
191	ATC GAA GTC ATC AAC CCG CGC CTT GCC GGC GGC GAA GAC GTG GCG GAC			970
192	Ile Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp			
193	290	295	300	
194				
195	CTG CGC GTT CGC TCC TCC ACG CTG AAG GGC GTC ACG GTG CCG GAA GAC			1018
196	Leu Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp			
197	305	310	315	
198				
199	CGC GCG CCT TCG ATG ATC GAC GAA TAT CCG ATT CTC GCT GTC GCC GCC			1066
200	Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala			
201	320	325	330	335
202				
203	GCC TTC GCG GAA GGG GCG ACC GTG ATG AAC GGT CTG GAA GAA CTC CGC			1114
204	Ala Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg			
205	340	345	350	

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206
207 GTC AAG GAA AGC GAC CGC CTC TCG GCC GTC GCC AAT GGC CTC AAG CTC 1162
208 Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu
209 355 360 365
210
211 AAT GGC GTG GAT TGC GAT GAG GGC GAG ACG TCG CTC GTC GTG CGC GGC 1210
212 Asn Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly
213 370 375 380
214
215 CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GCC GTC GCC 1258
216 Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala
217 385 390 395
218
219 ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC 1306
220 Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu
221 400 405 410 415
222
223 GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG 1354
224 Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr
225 420 425 430
226
227 AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC 1402
228 Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile
229 435 440 445
230
231 GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGGTC 1456
232 Glu Leu Ser Asp Thr Lys Ala Ala
233 450 455
234
235 CCGCTGCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTTTCATC 1516
236
237 ATCTCGATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCTGT 1576
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239 CGCTTGATGA CGAGGCGGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG 1636
240
241 ACCGGTCGGT GCTGTGCGCC CATGCCATCG GCGAGGCGGC TTCGAAGATC GCGGTCATGC 1696
242
243 CCTCGGTGCG GCGGGCGCTG GTCGAGGCGC AGCGCAGCTT TGCGGCGCGT GAGCCGGGCA 1756
244
245 CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCCC GGATGCGCCG GTGAAGCTCT 1816
246
247 ATGTCACCGC GTCACCGGAA GTGCGCGCGA AACGCCGCTA TGACGAAATC CTCGGCAATG 1876
248
249 GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA 1936
250
251 TGGGTCGGGC GGACAGTCCT TTGAAGCCCG CCGACGATGC GCACTT 1982
252
253
254 (2) INFORMATION FOR SEQ ID NO:3:
255
256 (i) SEQUENCE CHARACTERISTICS:
257 (A) LENGTH: 455 amino acids
258 (B) TYPE: amino acid

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text